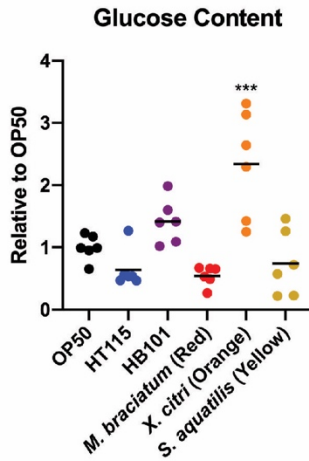


SUPPLEMENTAL FIGURES

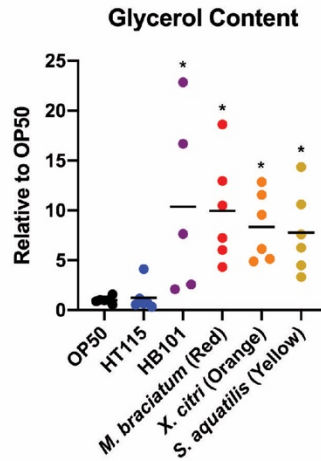
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Name	Bacteria	Doubling Time	Antibiotic Sensitivity	Growth Conditions for Experiments in Liquid Culture	Growth Conditions on Plate
OP50	<i>Escherichia coli</i>	2 Hours	Ampicillin	LB + Streptomycin at 37C	LB + Streptomycin at 37C
HT115	<i>Escherichia coli</i>	1 Hour	Streptomycin	LB + Ampicillin at 37C	LB + Ampicillin at 37C
HB101	<i>Escherichia coli</i>	3 Hours	Ampicillin	LB + Streptomycin at 37C	LB + Streptomycin at 37C
Red	<i>Methylobacterium</i>	23 Hours	Streptomycin	LB + Ampicillin at 37C	LB + Ampicillin at 30C
Orange	<i>Xanthomonas</i>	5 Hours	Streptomycin	LB + Ampicillin at 37C	LB + Kanamycin at 37C
Yellow	<i>Sphingomonas</i>	7 Hours	Streptomycin	LB + Ampicillin at 26C	LB + Ampicillin at 37C

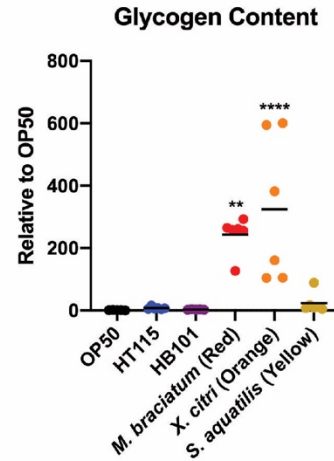
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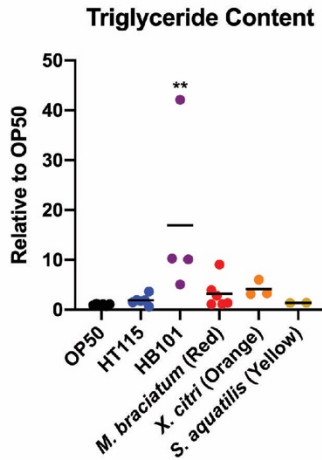
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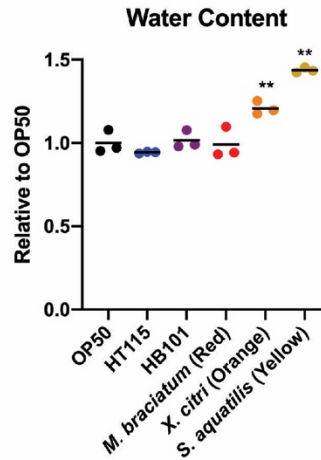
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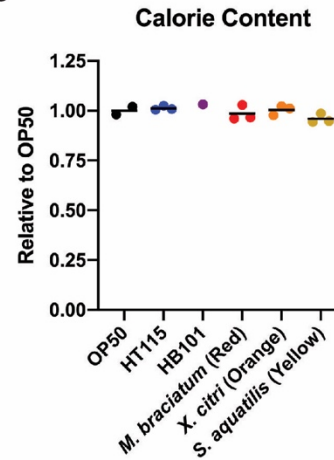
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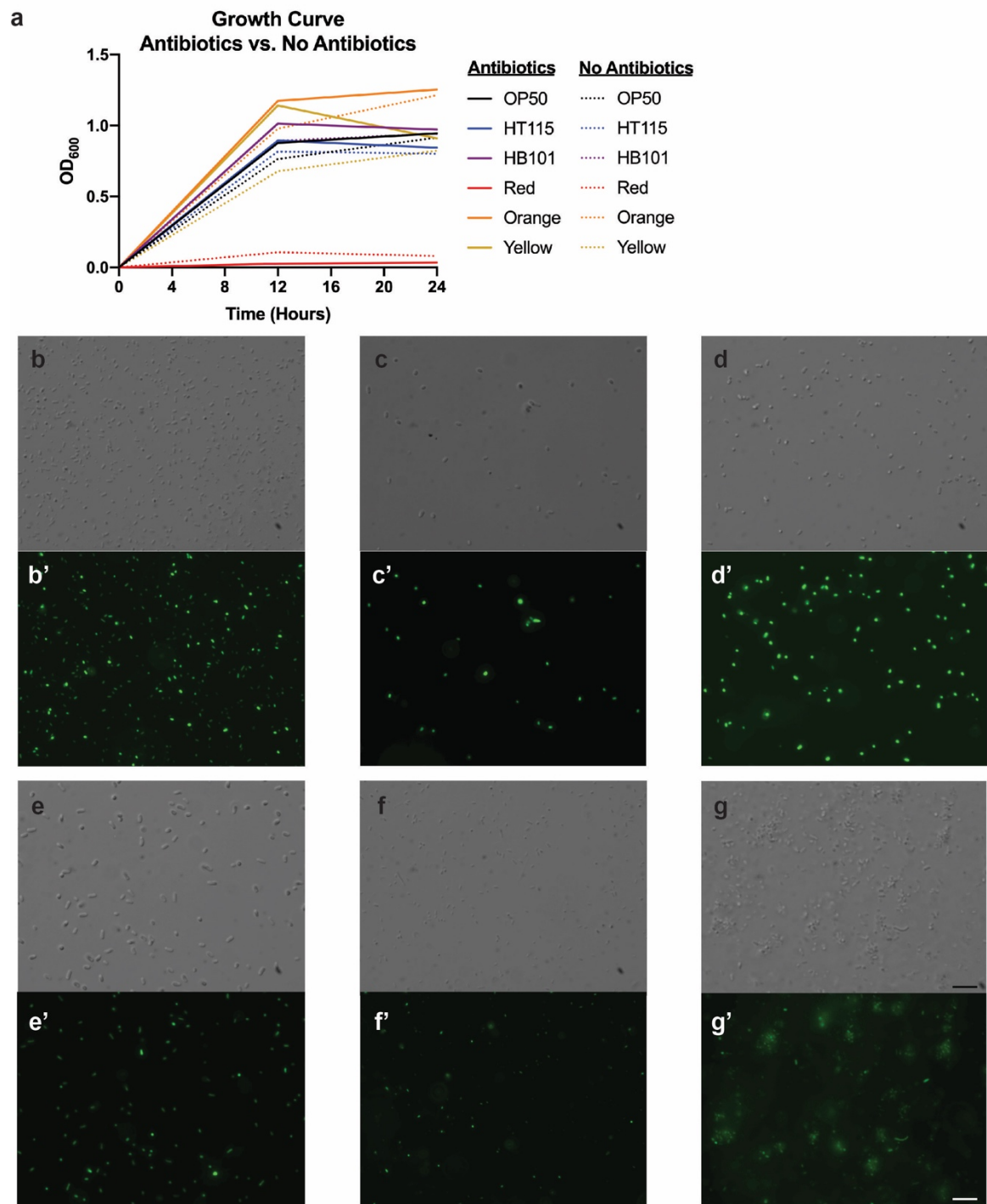
f



g



Supplemental Figure 1. Bacterial growth conditions and metabolite concentrations. (a) Table with optimal growth conditions for each bacterial diet. (b-g) Metabolite concentrations in each bacterium relative to OP50. The different metabolites measured were glucose (b), glycerol (c), glycogen (d), triglycerides (e) and water content (f). Statistical comparisons by Tukey's multiple comparison test. *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$; ****, $p < 0.0001$. All studies were performed in biological triplicate. (g) Calorie content of all bacteria were similar.

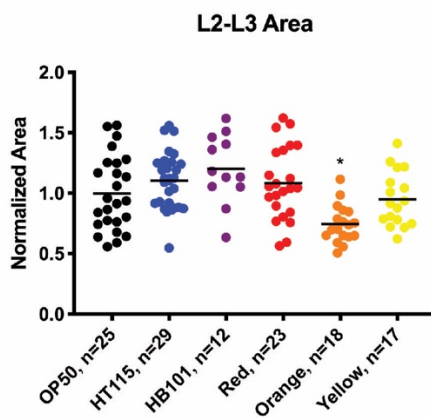


Supplemental Figure 2. Bacterial growth curve and images. (a) Bacterial growth curve comparison between growth in LB with and without antibiotics with no significant difference in growth rate. (b-g) Microscopic images of bacteria after being scraped off of a plate seeded at the optical density of 0.8 A_{600} . All bacteria are observably similar or smaller in size compared to OP50 bacteria. The bacteria are (b) OP50, (c) HT115, (d) HB101, (e) Red. (f) Orange, and (g) Yellow. (b'-g') Images of stained bacteria with BactoView™ Live Fluorescent dye that stains the DNA. Scale bar 5 μ m.

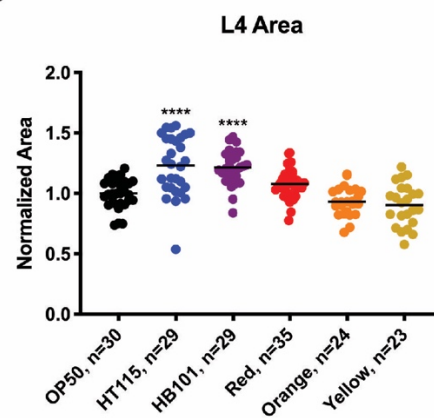
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Diet	Time to 50% of the Population Molting (Hours)				Total Time to Adulthood	Hours in each molt (Average number of hours worms were GFP positive)				% Faster than OP50-reared worms
	L1 Molt	L2 Molt	L3 Molt	L4 Molt		L1 Molt	L2 Molt	L3 Molt	L4 Molt	
OP50	11	22	30	41	50	6	4	6	7	-
HT115	11	18	27	38	44	9	3	5	6	20%
HB101	12	22	30	40	47	6	5	6	6	14.5%
Red	11	20	28	38	44	9	4	4	6	20%
Orange	13	23	29	39	46	5	3	4	5	16%
Yellow	13	22	30	40	46	5	3	4	4	16%

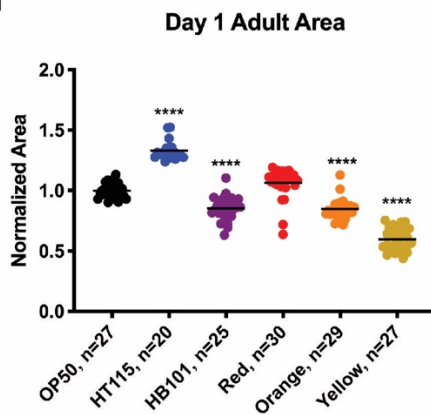
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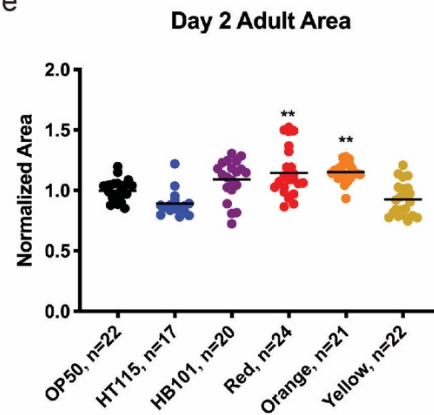
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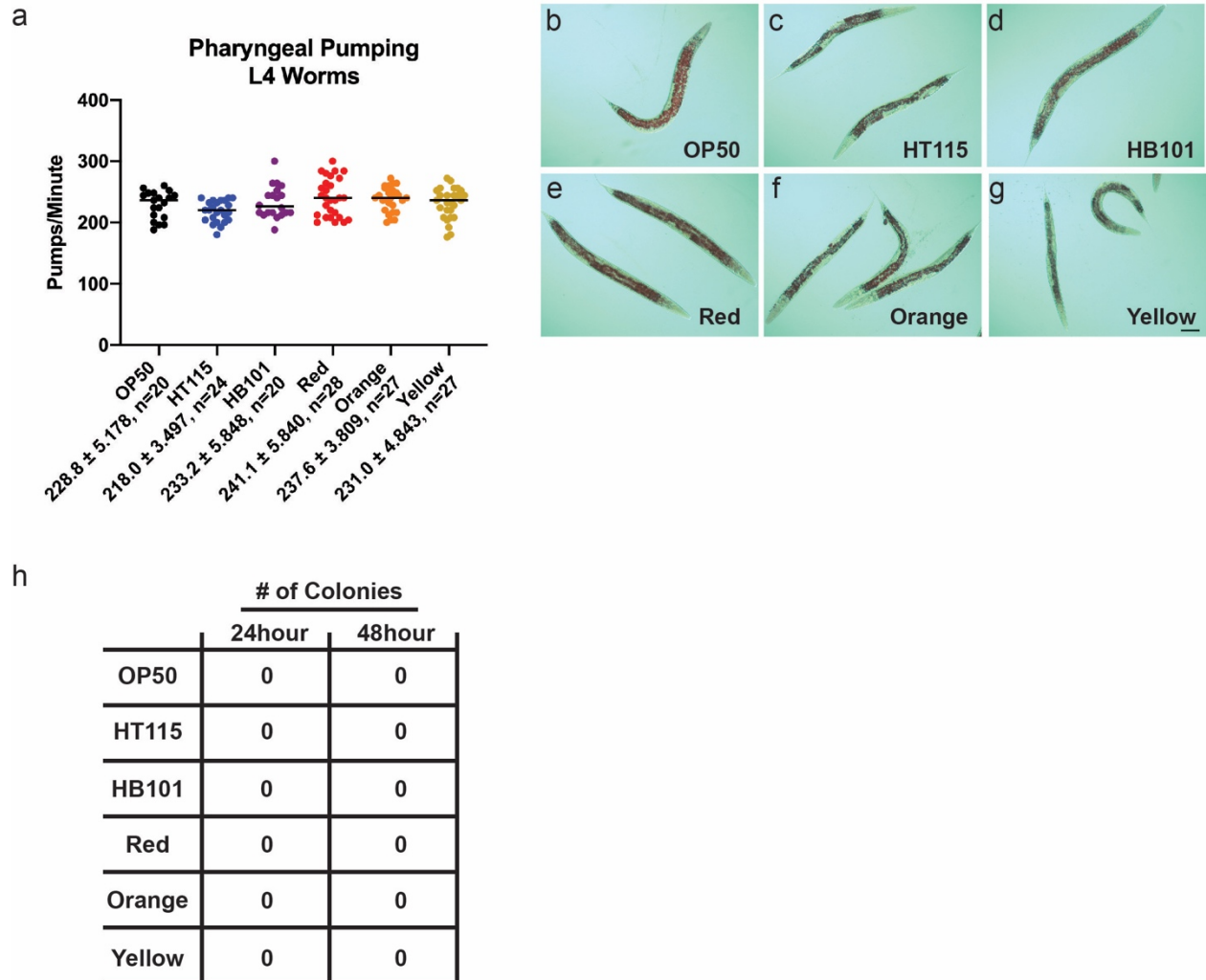
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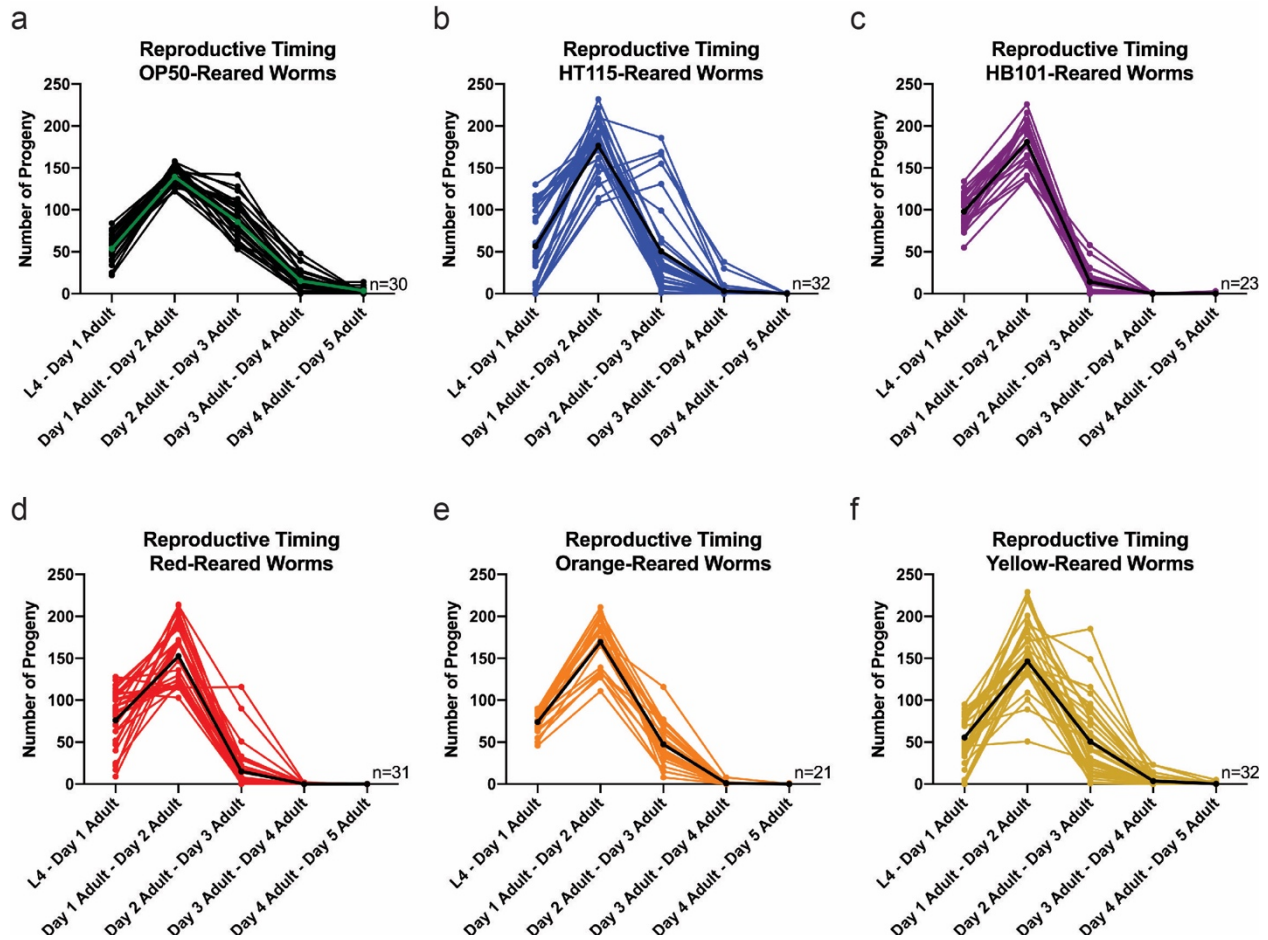
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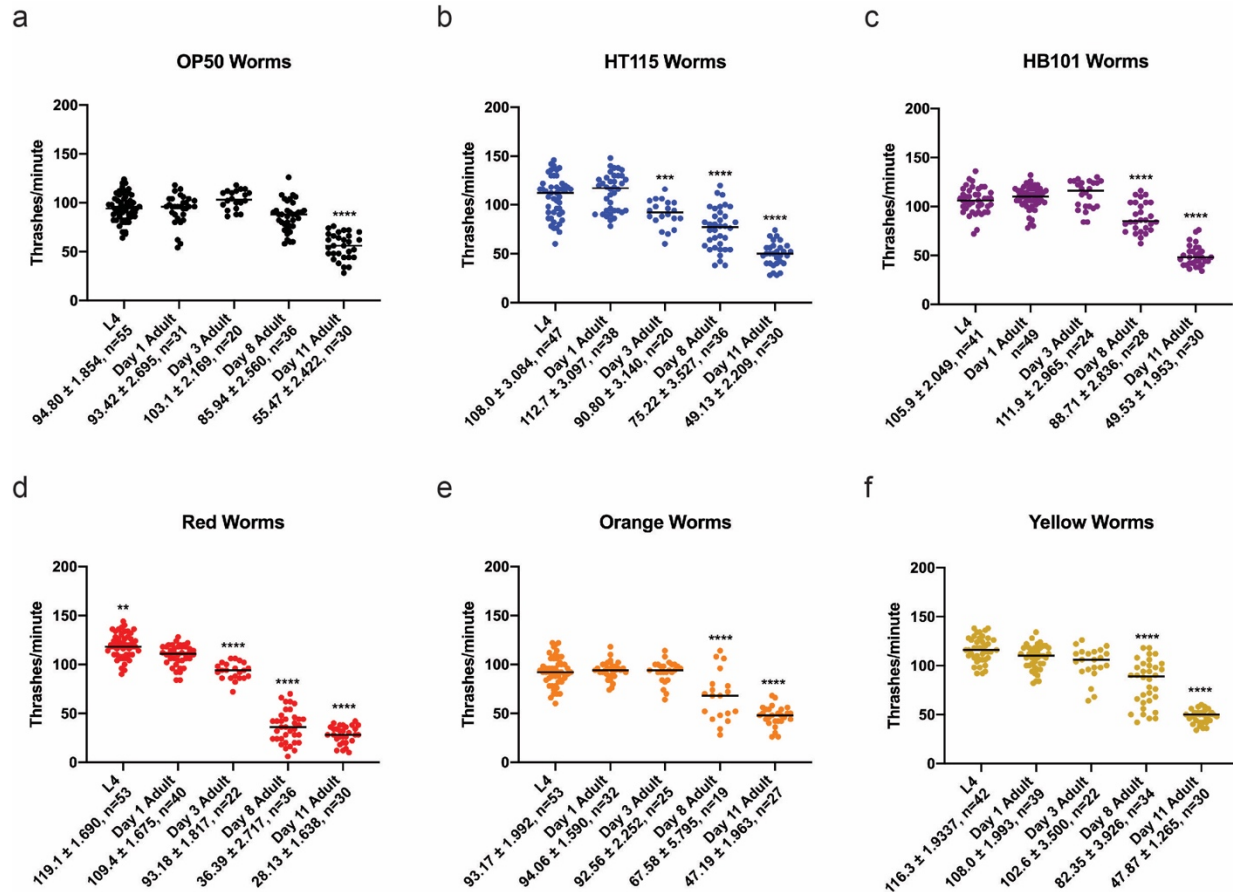
Supplemental Figure 3. Time in each developmental stage and worm area is altered based on bacterial diet raised on. (a) Table showing differences in time to each molt along with hours spend in each stage of development. (b-e) Area measurements of worms on each bacteria relative to OP50. (b) Orange-reared worms showed a slightly smaller area than OP50 and other bacteria. (c) *C. elegans* on HT115 and HB101 had significantly larger areas at the L4 stage. (d) Worms raised on HT115 have a larger area than worms raised on OP50 at day 1 of adulthood. HB101, Orange and Yellow worms have smaller area at day 1 of adulthood. (e) *C. elegans* raised on Red and Orange have larger areas at day 2 of adulthood compared to OP50 and the other diets. Statistical comparisons by Tukey's multiple comparison test. *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$; ****, $p < 0.0001$. All studies were performed in biological triplicate.



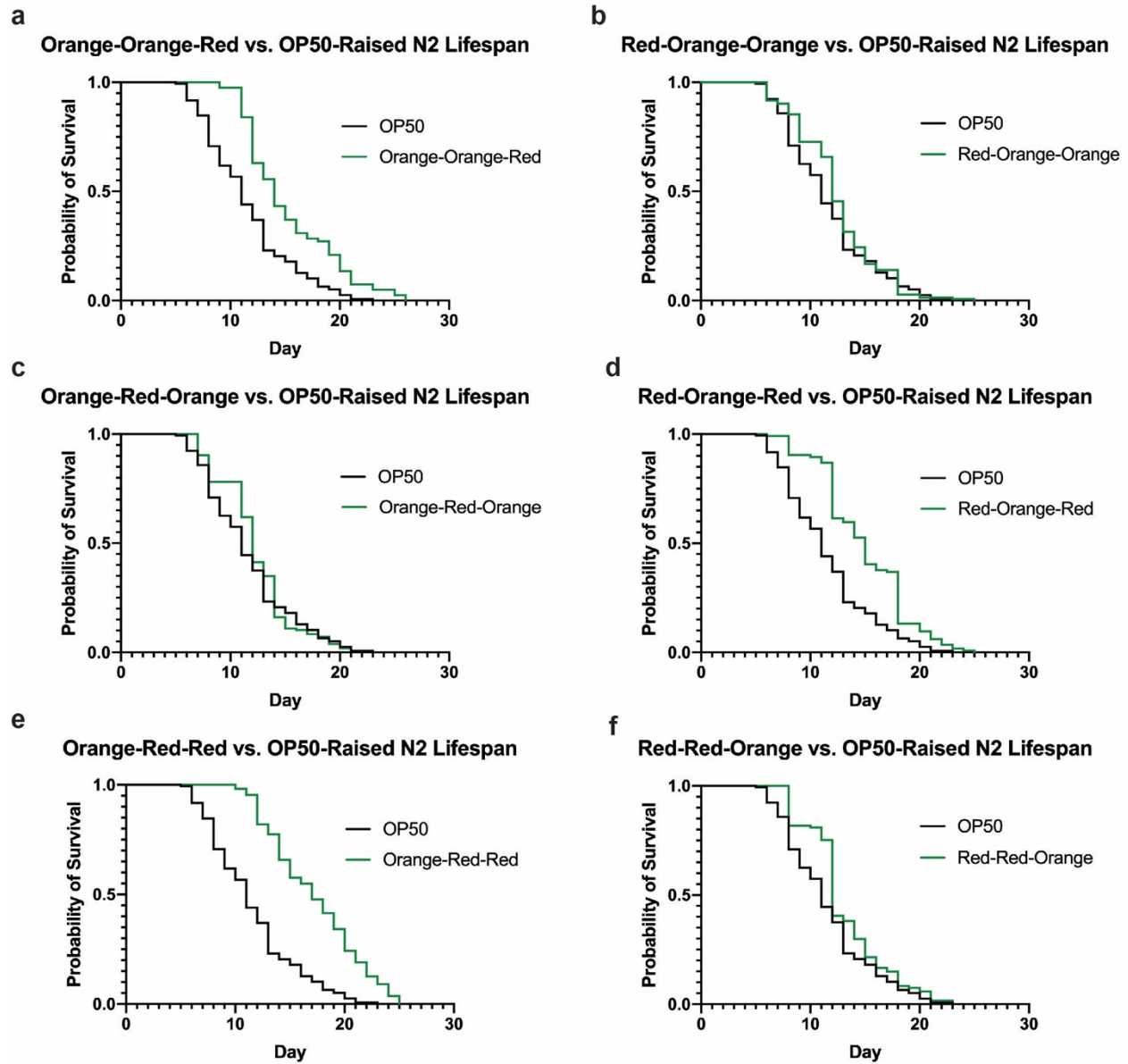
Supplemental Figure 4. L4 Pumping and Oil Red O staining. (a) L4 pumping of worms raised on each bacterial diet. There was no significant difference between worms raised on the different diets. Statistical comparisons by Tukey's multiple comparison test. Study was performed in biological triplicate. (b-g) Oil Red O staining for lipid distribution in L4 *C. elegans*. Scale bar 50 μ m. (h) Bacterial load experiment that counted the number of colonies that grew on an LB plate after 24 and 48 hours. n=48 individual worms per bacterial food.



Supplemental Figure 5 Reproductive timing is altered in *C. elegans* raised on the different bacterial diets. Reproductive output of individual worms (each line represents a different worm) at each day of its reproductive span. The thicker green line (a) and black line (b-f) on the graph represents the average output per day of reproduction. Worms were moved every 24 hours and progeny were counted. Each bacterial food had a reproductive peak from day 1 to day 2 of adulthood and then started producing fewer progeny per day until day 5 of adulthood. HB101 (c) and Red (d) worms have a significant decline in reproductive output by day 3 of adulthood.



Supplemental Figure 6 Thrashing declines with age in a food-dependent manner. C. *elegans* at each stage of development on each bacterial diet. Comparisons were made to day 1 of adulthood. Statistical comparisons by Tukey's multiple comparison test. *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$; ****, $p < 0.0001$. All studies were performed in biological triplicate. (a) OP50 thrashing starts to show a decline at day 11 of adulthood. (b) HT115 thrashing declines starting at day 3 of adulthood and continues to do so up until day 11 of adulthood. (c, e-f) HB101, Orange, and Yellow decline in thrashing rate at day 8 of adulthood and continues into day 11 of adulthood. (d) Red worms decline in thrashing from day 1 to day 11 of adulthood. Red-reared worms have the most significant rate of decline in thrashing compared to the other diets.



Supplemental Figure 7 Bacterial diet combinations compared to *C. elegans* raised on OP50. Lifespan comparisons of OP50 versus each nutraceutical diet combination. Lifespan comparisons made with Log-rank test (supplementary data 4).

SUPPLEMENTARY TABLES

Table S1. Gene Ontology (GO) Terms for RNAseq analysis in L4 *C. elegans* on bacterial diets.

HT115-specific	HB101-specific	Red-specific	Orange-specific	Yellow-specific
<p>GO-TERMS UP</p> <ul style="list-style-type: none"> organic acid metabolic process supramolecular polymer nucleoside phosphate binding ribonucleotide binding purine nucleotide binding nucleoside phosphate metabolic process purine nucleotide metabolic process ribose phosphate metabolic process actin filament-based process lipid catabolic process calcium ion binding hydrolase activity acting on acid anhydrides phosphorus metabolic process identical protein binding kinase binding <p>GO-TERMS DOWN</p> <ul style="list-style-type: none"> lipid catabolic process organic acid metabolic process 	<p>GO-TERMS UP</p> <ul style="list-style-type: none"> transmembrane transport establishment of localization metalloendopeptidase activity purine nucleotide binding supramolecular polymer nucleoside phosphate binding ribonucleotide binding structural constituent of cuticle peptidyl-tyrosine modification peptidyl-serine modification 	<p>GO-TERMS UP</p> <ul style="list-style-type: none"> immune system process defense response response to biotic stimulus phosphorus metabolic process 	<p>GO-TERMS DOWN</p> <ul style="list-style-type: none"> organic acid metabolic process lipid catabolic process 	<p>GO-TERMS UP</p> <ul style="list-style-type: none"> peptidyl-tyrosine modification extracellular space phosphorus metabolic process neuropeptide signaling pathway localization of cell protein modification process potassium ion transmembrane transport peptidyl-serine modification zinc ion binding intrinsic component of membrane dephosphorylation positive regulation of kinase activity metalloendopeptidase activity synaptic signaling peptidase activity <p>GO-TERMS DOWN</p> <ul style="list-style-type: none"> meiotic cell cycle organelle fission reproduction chromosome segregation cellular aromatic compound metabolic process heterocycle metabolic process membrane-enclosed lumen embryo development ending in birth or egg hatching organic cyclic compound metabolic process ribonucleoprotein granule RNA splicing via transesterification reactions modification-dependent macromolecule protein ubiquitination organelle covalent chromatin modification post-embryonic animal organ development cellular macromolecule localization negative regulation of metabolic process protein modification process protein catabolic process kinase binding regulation of protein metabolic process reproductive system development post-embryonic development development of primary sexual characteristics identical protein binding cellular developmental process transcription factor complex hydrolase activity acting on acid anhydrides macromolecule biosynthetic process regulation of nucleobase-containing compound methylation aging small GTPase binding process utilizing autophagic mechanism amide transport double-stranded DNA binding male anatomical structure morphogenesis oviposition